SEQUENCE LISTING

<110> Sakowicz, Roman
Goldstein, Lawrence S. B.
The Regents of the University of California

<120> Identification and Expression of a Novel Kinesin Motor Protein

<130> 18557C-000710US

<140> US 09/235,416
<141> 1999-01-22

<150> WO PCT/US99/01355
<151> 1999-01-22

<150> US 60/072,361
<151> 1998-01-23

<160> 7

<170> PatentIn Ver. 2.0

<210> 1
<211> 784
<212> PRT
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed microtubule motor protein

<220>
<221> DOMAIN
<222> (1)..(357)
<223> kinesin-like microtubule motor domain

<220>
<221> DOMAIN
<222> (358)..(442)
<223> neck domain links motor domain to stalk domain

<220>
<221> DOMAIN
<222> (443)..(601)
<223> stalk domain, unc-104 family domain

<220>
<221> DOMAIN
<222> (602)..(784)
<223> tail domain

<400> 1

```
Met Ser Gly Gly Gly Asn Ile Lys Val Val Val Arg Val Arg Pro Phe
 1               5                  10                  15

Asn Ala Arg Glu Ile Asp Arg Gly Ala Lys Cys Ile Val Arg Met Glu
            20                  25                  30
```

```
Gly Asn Gln Thr Ile Leu Thr Pro Pro Pro Gly Ala Glu Glu Lys Ala
        35                  40                  45

Arg Lys Ser Gly Lys Thr Ile Met Asp Gly Pro Lys Ala Phe Ala Phe
    50                  55                  60

Asp Arg Ser Tyr Trp Ser Phe Asp Lys Asn Ala Pro Asn Tyr Ala Arg
65                  70                  75                  80

Gln Glu Asp Leu Phe Gln Asp Leu Gly Val Pro Leu Leu Asp Asn Ala
                85                  90                  95

Phe Lys Gly Tyr Asn Asn Cys Ile Phe Ala Tyr Gly Gln Thr Gly Ser
            100                 105                 110

Gly Lys Ser Tyr Ser Met Met Gly Tyr Gly Lys Glu His Gly Val Ile
        115                 120                 125

Pro Arg Ile Cys Gln Asp Met Phe Arg Arg Ile Asn Glu Leu Gln Lys
    130                 135                 140

Asp Lys Asn Leu Thr Cys Thr Val Glu Val Ser Tyr Leu Glu Ile Tyr
145                 150                 155                 160

Asn Glu Arg Val Arg Asp Leu Leu Asn Pro Ser Thr Lys Gly Asn Leu
                165                 170                 175

Lys Val Arg Glu His Pro Ser Thr Gly Pro Tyr Val Glu Asp Leu Ala
            180                 185                 190

Lys Leu Val Val Arg Ser Phe Gln Glu Ile Glu Asn Leu Met Asp Glu
        195                 200                 205

Gly Asn Lys Ala Arg Thr Val Ala Ala Thr Asn Met Asn Glu Thr Ser
    210                 215                 220

Ser Arg Ser His Ala Val Phe Thr Leu Thr Leu Thr Gln Lys Trp His
225                 230                 235                 240

Asp Glu Glu Thr Lys Met Asp Thr Glu Lys Val Ala Lys Ile Ser Leu
                245                 250                 255

Val Asp Leu Ala Gly Ser Glu Arg Ala Thr Ser Thr Gly Ala Thr Gly
            260                 265                 270

Ala Arg Leu Lys Glu Gly Ala Glu Ile Asn Arg Ser Leu Ser Thr Leu
        275                 280                 285

Gly Arg Val Ile Ala Ala Leu Ala Asp Met Ser Ser Gly Lys Gln Lys
    290                 295                 300

Lys Asn Gln Leu Val Pro Tyr Arg Asp Ser Val Leu Thr Trp Leu Leu
305                 310                 315                 320

Lys Asp Ser Leu Gly Gly Asn Ser Met Thr Ala Met Ile Ala Ala Ile
                325                 330                 335

Ser Pro Ala Asp Ile Asn Phe Glu Glu Thr Leu Ser Thr Leu Arg Tyr
            340                 345                 350
```

```
Ala Asp Ser Ala Lys Arg Ile Lys Asn His Ala Val Val Asn Glu Asp
        355                 360                 365

Pro Asn Ala Arg Met Ile Arg Glu Leu Lys Glu Glu Leu Ala Gln Leu
    370                 375                 380

Arg Ser Lys Leu Gln Ser Ser Gly Gly Gly Gly Gly Gly Ala Gly Gly
385                 390                 395                 400

Ser Gly Gly Pro Val Glu Glu Ser Tyr Pro Pro Asp Thr Pro Leu Glu
                405                 410                 415

Lys Gln Ile Val Ser Ile Gln Gln Pro Asp Ala Thr Val Lys Lys Met
            420                 425                 430

Ser Lys Ala Glu Ile Val Glu Gln Leu Asn Gln Ser Glu Lys Leu Tyr
        435                 440                 445

Arg Asp Leu Asn Gln Thr Trp Glu Glu Lys Leu Ala Lys Thr Glu Glu
    450                 455                 460

Ile His Lys Glu Arg Glu Ala Ala Leu Glu Glu Leu Gly Ile Ser Ile
465                 470                 475                 480

Glu Lys Gly Phe Val Gly Pro Tyr His Ser Lys Glu Met Pro His Leu
                485                 490                 495

Val Asn Leu Ser Asp Asp Pro Leu Leu Ala Glu Cys Leu Val Tyr Asn
            500                 505                 510

Ile Lys Pro Gly Gln Thr Arg Val Gly Asn Val Asn Gln Asp Thr Gln
        515                 520                 525

Ala Glu Ile Arg Leu Asn Gly Ser Lys Ile Leu Lys Glu His Cys Thr
    530                 535                 540

Phe Glu Asn Val Asp Asn Val Val Thr Ile Val Pro Asn Glu Lys Ala
545                 550                 555                 560

Ala Val Met Val Asn Gly Val Arg Ile Asp Lys Pro Thr Arg Leu Arg
                565                 570                 575

Ser Gly Tyr Arg Ile Ile Leu Gly Asp Phe His Ile Phe Arg Phe Asn
            580                 585                 590

His Pro Glu Glu Ala Arg Ala Glu Arg Gln Glu Gln Ser Leu Leu Arg
        595                 600                 605

His Ser Val Thr Asn Ser Gln Leu Gly Ser Pro Ala Pro Gly Arg His
    610                 615                 620

Asp Arg Thr Leu Ser Lys Ala Gly Ser Asp Ala Asp Gly Asp Ser Arg
625                 630                 635                 640

Ser Asp Ser Pro Leu Pro His Phe Arg Gly Lys Asp Ser Asp Trp Phe
                645                 650                 655

Tyr Ala Arg Arg Glu Ala Ala Ser Ala Ile Leu Gly Leu Asp Gln Lys
            660                 665                 670
```

Ile Ser His Leu Thr Asp Asp Glu Leu Asp Ala Leu Phe Asp Asp Val
675 680 685

Gln Lys Ala Arg Ala Val Arg Arg Gly Leu Val Glu Asp Asn Glu Asp
690 695 700

Ser Asp Ser Gln Ser Ser Phe Pro Val Arg Asp Lys Tyr Met Ser Asn
705 710 715 720

Gly Thr Ile Asp Asn Phe Ser Leu Asp Thr Ala Ile Thr Met Pro Gly
725 730 735

Thr Pro Arg Ser Asp Asp Asp Gly Asp Ala Leu Phe Phe Gly Asp Lys
740 745 750

Lys Ser Lys Gln Asp Ala Ser Asn Val Asp Val Glu Glu Leu Arg Gln
755 760 765

Gln Gln Ala Gln Met Glu Glu Ala Leu Lys Thr Ala Lys Gln Glu Phe
770 775 780

<210> 2
<211> 2352
<212> DNA
<213> Thermomyces lanuginosus

<220>
<223> TL-gamma ATP-dependent plus end-directed
microtubule motor protein

<400> 2
atgtcgggcg gtggaaatat caaggtggtg gtgcgggtac gcccgttcaa cgcccgagaa 60
atcgaccgtg gcgcaaaatg tattgtgcgg atggaaggaa atcaaaccat cctcaccct 120
cctccgggtg ccgaagagaa ggcgcgtaaa agtggcaaaa ctattatgga tggcccgaag 180
gcatttgcgt tcgatcggtc gtattggtcc tttgacaaga atgctcccaa ctatgcgaga 240
caggaagacc tattccaaga tctcggagtc ccgcttctgg ataatgcatt caagggttat 300
aacaattgta tcttcgccta cggtcagacc ggttcgggca agtcctattc aatgatgggc 360
tatggcaagg agcatggcgt gatcccgcgg atttgccagg acatgttccg gcgtattaat 420
gaactgcaga aggacaagaa cctcacttgc accgtcgaag tttcgtactt ggaaatttac 480
aatgaacgag tgcgagactt gctgaatccg tcgacaaagg ggaatctcaa ggtccgagaa 540
cacccgtcga ccggccccta cgtggaggac ttggcgaagc tggtcgtgcg atcattccaa 600
gaaatcgaaa atctcatgga tgagggcaac aaagccagaa cggttgccgc cacaaacatg 660
aacgagacat ccagtcgatc ccacgccgtc ttcactttga ccttgacgca aaagtggcat 720
gatgaagaga ccaaaatgga cacagagaag gttgcgaaga tcagtctggt agatttggcg 780
ggttctgagc gagcaacgtc caccggagct actggagcgc gactgaagga gggtgcagag 840
atcaaccgct cactttcgac cctaggtcgt gtgattgcag cgctagcgga tatgtcgtcg 900
ggaaaacaga agaagaatca gttagtacct taccgagatt cggtactgac gtggcttctg 960
aaggactcct tgggaggcaa ctcgatgacc gccatgattg ccgccatttc gcctgctgat 1020
attaactttg aagagactct cagtaccctt cgatatgcgg actctgcgaa gcgaatcaag 1080
aaccacgcag tggtcaatga agacccgaac gcgcggatga tccgcgagtt gaaggaggaa 1140
ctcgcgcagc tgaggagcaa actccagagc agtggtggag gtggaggtgg tgcaggaggt 1200
tctggcgggc cagtggagga atcgtacccg cccgacacgc cgctcgagaa gcaaatcgtg 1260
tcgattcagc agccggatgc gacagtcaag aaaatgagca aggcagaaat cgtggagcaa 1320
ctgaaccaga gtgagaagct ctatcgggat ctcaatcaga cctgggaaga gaagctggcc 1380
aagaccgagg aaatccacaa ggaacgagaa gcggcgctcg aggagctggg tatcagcatc 1440
gaaaagggct ttgttggccc ttaccactcc aaagaaatgc cacatctagt caacttgagc 1500
gatgatcctc ttctggctga gtgtcttgtc tacaacatca agcccgggca gacaagggtt 1560
ggaaacgtca accaagatac acaagcggaa attcgtctga acggttcgaa gatcctgaaa 1620
gaacactgta cgtttgaaaa tgtggacaac gttgtgacca tcgtgccaaa cgagaaggct 1680
gctgtcatgg tgaacggcgt gcgaatcgac aagcctactc gcctccgcag cggctacagg 1740

atcatcctgg gcgatttcca cattttcga ttcaaccatc cggaagaagc tcgtgcggaa 1800
cggcaagaac aatccttgct tcgccattct gtcaccaaca gtcagttggg ttcgcctgct 1860
ccaggccgtc acgaccggac actgagcaag gcgggttcgg atgcggacgg cgattctcgc 1920
tcagattctc ctttgccgca ctttcgtgga aaggatagcg actggttcta tgctcgcagg 1980
gaagctgcta gcgcgatcct agggttggat cagaagatct ctcatctgac agatgacgag 2040
ttggatgcat tatttgacga tgttcagaaa gcgcgggcag ttcgtcgtgg gctggtcgaa 2100
gacaacgaag atagcgattc gcagagttcg tttccggtcc gtgacaaata catgtccaat 2160
ggaaccattg ataatttctc gctcgatacc gccattacta tgccgggtac ccctcgtagt 2220
gatgacgacg gtgacgcgct gttttttggt gataagaagt cgaaacagga tgcgtctaat 2280
gttgatgttg aggagttgcg tcaacagcag gctcagatgg aagaagccct gaaaacagcg 2340
aagcaggaat tc 2352

<210> 3
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 3
atgtcgggcg gtggaaatat c 21

<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:primer

<400> 4
gaattcctgc ttcgctgttt tca 23

<210> 5
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
forward primer

<220>
<221> modified_base
<222> (25)
<223> n = a, c, g or t

<400> 5
gcgcggatcc atyttygcht ayggncarac 30

<210> 6
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
reverse primer

<220>
<221> modified_base
<222> (16)
<223> n = a, c, g or t

<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t

<400> 6
gcgcgaattc tcdganccdg cvarrtcnac 30

<210> 7
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:degenerate
reverse primer

<220>
<221> modified_base
<222> (16)
<223> n = a, c, g or t

<220>
<221> modified_base
<222> (28)
<223> n = a, c, g or t

<400> 7
gcgcgaattc tcdctnccdg cvarrtcnac 30